

SEQUENCE LISTING

<110> Laus, Reiner
Vidovic, Damir
Graddis, Thomas

<120> Compositions and Methods for Dendritic
Cell-Based Immunotherapy

<130> 7636-0022.30

<140> Not Yet Assigned

<141> Filed Herewith

<150> US 60/193,504

<151> 2000-03-30

<160> 30

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 555

<212> PRT

<213> Artificial Sequence

<220>

<223> HER500 construct

<400> 1

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Lys	Glu	Leu	Ala	Arg	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr
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Asp	Met	Lys	Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met
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Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile
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Gln	Glu	Val	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln
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Val	Pro	Leu	Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu
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Asp	Asn	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn
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Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln
145				150					155					160	
Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg
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Asn	Pro	Gln	Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe
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His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser

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				165					170					175	
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			180					185					190		
His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser
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Glu	Gln	Cys	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu
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Ala	Cys	Leu	His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro
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Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	Ala	Ser	Ile	Ile	Asn	Phe	Glu
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Lys	Leu	Gly	Ala	Gly	Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	Ser
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Ser	Leu	Pro	Thr	His	Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp
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Pro	Thr	Val	Pro	Leu	Pro	Ser	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu
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Thr	Cys	Ser	Pro	Gln	Pro	Glu	Tyr	Val	Asn	Gln	Pro	Asp	Val	Arg	Pro
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Val	Val	Lys	Asp	Val	Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu
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Tyr	Leu	Thr	Pro	Gln	Gly	Gly	Ala	Ala	Pro	Gln	Pro	His	Pro	Pro	Pro
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Ala	Phe	Ser	Pro	Ala	Phe	Asp	Asn	Leu	Tyr	Tyr	Trp	Asp	Gln	Asp	Pro
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Pro	Glu	Arg	Gly	Ala	Pro	Pro	Ser	Thr	Phe	Lys	Gly	Thr	Pro	Thr	Ala
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His	His	His	His												

<210> 4

<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> HER500*-rGM-CSF construct

<400> 4

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 20          25          30
Lys Glu Leu Ala Arg Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr
 35          40          45
Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
 50          55          60
Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu
 65          70          75          80
Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile
 85          90          95
Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln
100          105          110
Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu
115          120          125
Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn
130          135          140
Thr Thr Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln
145          150          155          160
Leu Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg
165          170          175
Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe
180          185          190
His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser
195          200          205
Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp
210          215          220
Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala
225          230          235          240
Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His
245          250          255
Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu
260          265          270
Ala Cys Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro
275          280          285
Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro
290          295          300
Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr
305          310          315          320
Asn Tyr Leu Ser Thr Asp Val Gly Ser Ala Ser Ile Ile Asn Phe Glu
325          330          335
Lys Leu Gly Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser
340          345          350
Thr Arg Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu
355          360          365
Glu Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser
370          375          380
Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln
385          390          395          400
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Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp
 405 410 415
 Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu
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 Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro
 435 440 445
 Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala
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 Gly Ala Thr Leu Glu Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly
 465 470 475 480
 Val Val Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu
 485 490 495
 Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro
 500 505 510
 Ala Phe Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro
 515 520 525
 Pro Glu Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala
 530 535 540
 Glu Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro Ala Ala Ala Pro Thr
 545 550 555 560
 Arg Ser Pro Asn Pro Val Thr Arg Pro Trp Lys His Val Asp Ala Ile
 565 570 575
 Lys Glu Ala Leu Ser Leu Leu Asn Asp Met Arg Ala Leu Glu Asn Glu
 580 585 590
 Lys Asn Glu Asp Val Asp Ile Ile Ser Asn Glu Phe Ser Ile Gln Arg
 595 600 605
 Pro Thr Cys Val Gln Thr Arg Leu Lys Leu Tyr Lys Gln Gly Leu Arg
 610 615 620
 Gly Asn Leu Thr Lys Leu Asn Gly Ala Leu Thr Met Ile Ala Ser His
 625 630 635 640
 Tyr Gln Thr Asn Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Ile Glu
 645 650 655
 Val Thr Thr Phe Glu Asp Phe Ile Lys Asn Leu Lys Gly Phe Leu Phe
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 Pro Pro Ala His His His His His His
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<210> 5

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> HER300*-rGM-CSF construct

<400> 5

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 Lys Glu Leu Ala Arg Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr
 35 40 45
 Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
 50 55 60
 Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu

65					70					75					80
Leu	Thr	Tyr	Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile
				85					90					95	
Gln	Glu	Val	Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln
			100					105					110		
Val	Pro	Leu	Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu
		115					120					125			
Asp	Asn	Tyr	Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn
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Thr	Thr	Pro	Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln
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Leu	Arg	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg
			165						170					175	
Asn	Pro	Gln	Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe
		180					185						190		
His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser
		195					200					205			
Arg	Ala	Cys	His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp
		210				215					220				
Gly	Glu	Ser	Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala
225					230					235					240
Gly	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His
			245						250					255	
Glu	Gln	Cys	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu
			260					265					270		
Ala	Cys	Leu	His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro
		275					280					285			
Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro
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Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr
305					310					315					320
Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	Ala	Ser	Ile	Ile	Asn	Phe	Glu
			325						330					335	
Lys	Leu	Ala	Ala	Pro	Thr	Arg	Ser	Pro	Asn	Pro	Val	Thr	Arg	Pro	Trp
		340					345						350		
Lys	His	Val	Asp	Ala	Ile	Lys	Glu	Ala	Leu	Ser	Leu	Leu	Asn	Asp	Met
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Arg	Ala	Leu	Glu	Asn	Glu	Lys	Asn	Glu	Asp	Val	Asp	Ile	Ile	Ser	Asn
		370				375					380				
Glu	Phe	Ser	Ile	Gln	Arg	Pro	Thr	Cys	Val	Gln	Thr	Arg	Leu	Lys	Leu
385					390					395					400
Tyr	Lys	Gln	Gly	Leu	Arg	Gly	Asn	Leu	Thr	Lys	Leu	Asn	Gly	Ala	Leu
			405						410					415	
Thr	Met	Ile	Ala	Ser	His	Tyr	Gln	Thr	Asn	Cys	Pro	Pro	Thr	Pro	Glu
			420					425					430		
Thr	Asp	Cys	Glu	Ile	Glu	Val	Thr	Phe	Glu	Asp	Phe	Ile	Lys	Asn	
		435					440				445				
Leu	Lys	Gly	Phe	Leu	Phe	Asp	Ile	Pro	Phe	Asp	Cys	Trp	Lys	Pro	Val
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 <211> 1665
 <212> DNA
 <213> Artificial Sequence

<220>

<223> HER500 construct

<400> 6

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<210> 7

<211> 2070

<212> DNA

<213> Artificial Sequence

<220>

<223> HER500-hGM-CSF construct

<400> 7

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<210> 8

<211> 1692

<212> DNA

<213> Artificial Sequence

<220>

<223> HER500* construct

<400> 8

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ggctacgtgc	tcctcgtctc	caaccaagt	aggcaggtcc	cactgcagag	gctgcggatt	360
gtgcgaggca	cccagctctt	tgaggacaac	tatgccctgg	ccgtgctaga	caatggagac	420
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gtcgtcaaa	acgtttttgc	ctttgggggt	gccgtggaga	accccagta	cttgacaccc	1500
cagggaggag	ctgcccctca	gccccaccct	cctcctgcct	tcagcccagc	cttcgacaac	1560
ctctattact	gggaccagga	cccaccagag	cggggggctc	caccacagcac	cttcaaaggg	1620

acacctacgg cagagaaccc agagtacctg ggtctggacg tgccagcggc cgcacatcac 1680
catcaccatc ac 1692

<210> 9
<211> 2091
<212> DNA
<213> Artificial Sequence

<220>
<223> HER500*-rGM-CSF construct

<400> 9
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tcgacccaag tgtgcaccgg cacagacatg aagctgcggc tccctgccag tcccagacc 180
cacctggaca tgtccgccca cctctaccag ggctgccagg tggcgaggg aaacctggaa 240
ctcacctacc tgccaccaaa tgccagcctg tcttctctgc aggatatcca ggaggtgcag 300
ggctacgtgc tcatcgctca caaccaagtg aggcaggctc cactgcagag gctgcggatt 360
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ccgctgaaca ataccacccc tgtcacaggg gcctccccag gaggcctgcg ggagctgcag 480
cttcgaagcc tcacagagat cttgaaagga ggggtcttga tccagcggaa cccccagctc 540
tgctaccagg acacgatttt gtggaaggac atcttccaca agaacaacca gctggctctc 600
acactgatag acaccaaccg ctctcgggcc tgccaccctt gttctccgat gtgtaagggc 660
tcccgtgct ggggagagag ttctgaggat tgtcagagcc tgacgcgcac tgtctgtgcc 720
ggtggtgtg cccgtgcaa ggggccactg cccactgact gctgccatga gcagtgtgct 780
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gcccagacct ctggtgccac tctggaaagg gccaaagactc tctccccagg gaagaatggg 1440
gtcgtcaaag acgtttttgc ctttgggggt gccgtggaga accccgagta cttgacacct 1500
cagggaggag ctgcccctca gccccaccct cctcctgcct tcagcccagc cttcgacaac 1560
ctctattact gggaccagga cccaccagag cggggggctc caccagcac cttcaaaggg 1620
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tctaagtgtg tctccatcca gagccgcaca tgtgtgcaga cccgcctgaa gctatacaag 1860
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gaggatttca taaagaacct taaaggcttt ctgtttgata tcccttttga ctgctggaag 2040
ccggtccaga aaggcgcgcc acccccgcgg gcgcacatcac atcaccatca c 2091

<210> 10
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> HER300*-rGM-CSF construct

<400> 10

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tcgaccaag tgtgcaccgg cacagacatg aagctgcggc tccctgccag tcccgagacc      180
cacctggaca tgctccgcca cctctaccag ggctgccagg tgggtgcagg aaacctggaa      240
ctcacctacc tgcccaccaa tgccagcctg tccttctctg aggatatcca ggaggtgcag      300
ggctacgtgc tcatcgctca caaccaagtg aggcaggtcc cactgcagag gctgcggatt      360
gtgcgaggca ccagctctt tgaggacaac tatgccctgg ccgtgctaga caatggagac      420
ccgctgaaca ataccacccc tgtcacaggg gcctccccag gaggcctgcg ggagctgcag      480
cttcgaagcc tcacagagat cttgaaagga ggggtcttga tccagcggaa ccccagctc      540
tgctaccagg acacgatttt gtggaaggac atcttccaca agaacaacca gctggctctc      600
acactgatag acaccaaccg ctctcggggc tgccacccct gttctccgat gtgtaagggc      660
tcccgtgct ggggagagag ttctgaggat tgtcagagcc tgacgcgcac tgtctgtgcc      720
ggtggctgtg cccgtgcaa ggggccactg cccactgact gctgccatga gcagtgtgct      780
gccggctgca cgggccccaa gcactctgac tgccctggcct gcctccactt caaccacagt      840
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atgccaatc ccgagggccg gtatacattc ggcgccagct gtgtgactgc ctgtccctac      960
aactacctt ctacggacgt gggatccgct agcatcatta atttcgagaa gttggccgcc      1020
cccaccgct caccacaacc tgtcaccgg ccctggaagc atgtagatgc catcaaagaa      1080
gctctgagcc tcctaaatga catgctgtgt ctggagaacg aaaagaacga agacgtagac      1140
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tacaagcagg gtctacgggg caacctcacc aaactcaatg gcgccttgac catgatagcc      1260
agccactacc agacgaactg cctccaacc ccggaaactg actgtgaaat agaagtcacc      1320
acctttgagg atttcataaa gaaccttaaa ggctttctgt ttgatatccc ttttgactgc      1380
tggaagccgg tccagaaagg cgcgccacc cgcgcggcgc atcaccatca ccatcac      1437

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<210> 11
<211> 32
<212> PRT
<213> Homo sapiens

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<400> 11
Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
  1             5             10             15
Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
      20             25             30

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<210> 12
<211> 3
<212> PRT
<213> Homo sapiens

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<400> 12
Lys Glu Leu
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<210> 13
<211> 3
<212> PRT
<213> Homo sapiens

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<400> 13
Gly Ala Ala
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<210> 14
<211> 2
<212> PRT

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<213> Artificial Sequence

<220>

<223> linker

<400> 14

Ala Arg

1

<210> 15

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> C-terminal sequence of HER500 and HER500* constructs

<400> 15

Ala Ala Ala His His His His His His

1

5

<210> 16

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> C-terminal sequence of HER500-hGM-CSF construct

<400> 16

Gly Ala Pro Pro Pro Pro Ala Ala Ala His His His His His His

1

5

10

15

<210> 17

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> C-terminal sequence of HER500* and HER300* rat GM-CSF constructs

<400> 17

Gly Ala Pro Pro Pro Pro Ala His His His His His His

1

5

10

<210> 18

<211> 127

<212> PRT

<213> Homo sapiens

<400> 18

Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val

1

5

10

15

Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr

20

25

30

Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe Asp
35 40 45
Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys Gln
50 55 60
Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met Met
65 70 75 80
Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser Cys
85 90 95
Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp
100 105 110
Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
115 120 125

<210> 19
<211> 381
<212> DNA
<213> Homo sapiens

<400> 19
gcacccgccc gctcgcccag cccagcacg cagccctggg agcatgtgaa tgccatccag 60
gaggcccggc gtctcctgaa cctgagtaga gacactgctg ctgagatgaa tgaaacagta 120
gaagtcattct cagaaatgtt tgacctccag gagccgacct gcctacagac ccgcctggag 180
ctgtacaagc agggcctgcg gggcagcctc accaagctca agggcccctt gaccatgatg 240
gccagccact acaagcagca ctgccctcca accccggaaa cttcctgtgc aaccagact 300
atcacctttg aaagtttcaa agagaacctg aaggactttc tgcttgatcat cccctttgac 360
tgctggggagc cagtccagga g 381

<210> 20
<211> 127
<212> PRT
<213> Rattus norvegicus

<400> 20
Ala Pro Thr Arg Ser Pro Asn Pro Val Thr Arg Pro Trp Lys His Val
1 5 10 15
Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asp Met Arg Ala Leu
20 25 30
Glu Asn Glu Lys Asn Glu Asp Val Asp Ile Ile Ser Asn Glu Phe Ser
35 40 45
Ile Gln Arg Pro Thr Cys Val Gln Thr Arg Leu Lys Leu Tyr Lys Gln
50 55 60
Gly Leu Arg Gly Asn Leu Thr Lys Leu Asn Gly Ala Leu Thr Met Ile
65 70 75 80
Ala Ser His Tyr Gln Thr Asn Cys Pro Pro Thr Pro Glu Thr Asp Cys
85 90 95
Glu Ile Glu Val Thr Thr Phe Glu Asp Phe Ile Lys Asn Leu Lys Gly
100 105 110
Phe Leu Phe Asp Ile Pro Phe Asp Cys Trp Lys Pro Val Gln Lys
115 120 125

<210> 21
<211> 381
<212> DNA
<213> Rattus norvegicus

<400> 21
gcacccaccc gctcacccaa ccctgtcacc cggccctgga agcatgtaga tgccatcaaa 60

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gaagctctga gcctcctaaa tgacatgcgt gctctggaga acgaaaagaa cgaagacgta 120
gacatcatct ctaatgagtt ctccatccag aggccgacat gtgtgcagac ccgcctgaag 180
ctatacaagc agggctctacg gggcaacctc accaaactca atggcgccctt gaccatgata 240
gccagccact accagacgaa ctgccctcca accccggaaa ctgactgtga aatagaagtc 300
accacctttg aggatttcat aaagaacctt aaaggctttc tgtttgatat cccttttgac 360
tgctggaagc cggtcagaa a 381

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<210> 22
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OVA-derived immunodominant octapeptide

<400> 22
 Ser Ile Ile Asn Phe Glu Lys Leu
 1 5

<210> 23
 <211> 289
 <212> PRT
 <213> Homo sapiens

<400> 23
 Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys Leu Arg Leu Pro Ala
 1 5 10 15
 Ser Pro Glu Thr His Leu Asp Met Leu Arg His Leu Tyr Gln Gly Cys
 20 25 30
 Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr Leu Pro Thr Asn Ala
 35 40 45
 Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val Gln Gly Tyr Val Leu
 50 55 60
 Ile Ala His Asn Gln Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile
 65 70 75 80
 Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu
 85 90 95
 Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser
 100 105 110
 Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu
 115 120 125
 Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp
 130 135 140
 Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn Asn Gln Leu Ala Leu
 145 150 155 160
 Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys His Pro Cys Ser Pro
 165 170 175
 Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser Ser Glu Asp Cys Gln
 180 185 190
 Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys Ala Arg Cys Lys Gly
 195 200 205
 Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys Ala Ala Gly Cys Thr
 210 215 220
 Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu His Phe Asn His Ser
 225 230 235 240
 Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val Thr Tyr Asn Thr Asp
 245 250 255

Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg Tyr Thr Phe Gly Ala
 260 265 270
 Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu Ser Thr Asp Val Gly
 275 280 285
 Ser

<210> 24
 <211> 867
 <212> DNA
 <213> Homo sapiens

<400> 24
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 cacctggaca tgctccgcca cctctaccag ggctgccagg tgggtgcaggg aaacctggaa 120
 ctcacctacc tgcccaccaa tgccagcctg tccttcctgc aggatatcca ggaggtgcag 180
 ggctacgtgc tcatcgctca caaccaagtg aggcagggtcc cactgcagag gctgcggatt 240
 gtgcgaggca cccagctctt tgaggacaac tatgccctgg ccgtgctaga caatggagac 300
 ccgctgaaca ataccacccc tgtcacaggg gcctcccagc gaggcctgcg ggagctgcag 360
 ctctgaagcc tcacagagat cttgaaagga ggggtcttga tccagcggaa cccccagctc 420
 tgctaccagg acacgatttt gtggaaggac atcttcacac agaacaacca gctggctctc 480
 aactgatag acaccaaccg ctctcggggc tgccaccctt gttctccgat gtgtaagggc 540
 tcccgtctgt ggggagagag ttctgaggat tgtcagagcc tgacgcgcac tgtctgtgcc 600
 ggtggctgtg cccgctgcaa ggggccactg cccactgact gctgccatga gcagtgtgct 660
 gccggtgtga cgggccccaa gcactctgac tgcttgccct gcctccactt caaccacagt 720
 ggcattctgt agctgcactg cccagccctg gtcacctaca acacagacac gtttgagtcc 780
 atgcccaatc ccgagggccg gtatacatc ggcgccagct gtgtgactgc ctgtccctac 840
 aactaccttt ctacggacgt gggatcc 867

<210> 25
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 25
 Gly Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg
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 Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu
 20 25 30
 Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val
 35 40 45
 Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu
 50 55 60
 Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr
 65 70 75 80
 Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys
 85 90 95
 Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro
 100 105 110
 Pro Ser Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala
 115 120 125
 Thr Leu Glu Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val
 130 135 140
 Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu
 145 150 155 160
 Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe
 165 170 175

Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu
180 185 190
Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn
195 200 205
Pro Glu Tyr Leu Gly Leu Asp Val Pro
210 215

<210> 26
<211> 651
<212> DNA
<213> Homo sapiens

<400> 26
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gacctgacac tagggctgga gccctctgaa gaggagggcc ccaggtctcc actggcacc 120
tccgaagggg ctgggtccga tgtatttgat ggtgacctgg gaatgggggc agccaagggg 180
ctgcaaagcc tccccacaca tgaccccagc cctctacagc ggtacagtga ggaccccaca 240
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aatggggctg tcaaagacgt ttttgccctt ggggggtgccg tggagaaccc cgagtacttg 480
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gacaacctct attactggga ccaggaccca ccagagcggg gggctccacc cagcaccttc 600
aaagggacac ctacggcaga gaaccagag tacctgggtc tggacgtgcc a 651

<210> 27
<211> 397
<212> PRT
<213> Artificial Sequence

<220>
<223> NY-ESO-IC tumor antigen

<400> 27
Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
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Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
20 25 30
Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45
Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
50 55 60
His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
65 70 75 80
Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
85 90 95
Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
100 105 110
Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
115 120 125
Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
130 135 140
Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
145 150 155 160
Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser
165 170 175
Gly Gln Arg Arg Gly Ala Gly Gly Met Val His His Arg His Arg Ser

<210> 29
 <211> 1179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SART-3-IC

<400> 29

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Lys	Ala	Gly	Pro	Lys	Ala	Asp	Gly	Glu	Glu	Asp	Glu	Val	Lys	Ala	Ala
			20					25					30		
Arg	Thr	Arg	Arg	Lys	Val	Leu	Ser	Arg	Ala	Val	Ala	Ala	Ala	Thr	Tyr
			35				40					45			
Lys	Thr	Met	Gly	Pro	Ala	Trp	Asp	Gln	Gln	Glu	Glu	Gly	Val	Ser	Glu
	50					55				60					
Ser	Asp	Gly	Asp	Glu	Tyr	Ala	Met	Ala	Ser	Ser	Ala	Glu	Ser	Ser	Pro
65					70				75						80
Gly	Glu	Tyr	Glu	Trp	Glu	Tyr	Asp	Glu	Glu	Glu	Glu	Lys	Asn	Gln	Leu
				85				90					95		
Glu	Ile	Glu	Arg	Leu	Glu	Glu	Gln	Leu	Ser	Ile	Asn	Val	Tyr	Asp	Tyr
			100				105					110			
Asn	Cys	His	Val	Asp	Leu	Ile	Arg	Leu	Leu	Arg	Leu	Glu	Gly	Glu	Leu
	115						120					125			
Thr	Lys	Val	Arg	Met	Ala	Arg	Gln	Lys	Met	Ser	Glu	Ile	Phe	Pro	Leu
	130					135					140				
Thr	Glu	Glu	Leu	Trp	Leu	Glu	Trp	Leu	His	Asp	Glu	Ile	Ser	Met	Ala
145					150					155					160
Gln	Asp	Gly	Leu	Asp	Arg	Glu	His	Val	Tyr	Asp	Leu	Phe	Glu	Lys	Ala
				165				170					175		
Val	Lys	Asp	Tyr	Ile	Cys	Pro	Asn	Ile	Trp	Leu	Glu	Tyr	Gly	Gln	Tyr
			180					185					190		
Ser	Val	Gly	Gly	Ile	Gly	Gln	Lys	Gly	Gly	Leu	Glu	Lys	Val	Arg	Ser
		195					200					205			
Val	Phe	Glu	Arg	Ala	Leu	Ser	Ser	Val	Gly	Leu	His	Met	Thr	Lys	Gly
	210					215					220				
Leu	Ala	Leu	Trp	Glu	Ala	Tyr	Arg	Glu	Phe	Glu	Ser	Ala	Ile	Val	Glu
225					230				235						240
Ala	Ala	Arg	Leu	Glu	Lys	Val	His	Ser	Leu	Phe	Arg	Arg	Gln	Leu	Ala
				245					250					255	
Ile	Pro	Leu	Tyr	Asp	Met	Glu	Ala	Thr	Phe	Ala	Glu	Tyr	Glu	Glu	Trp
			260					265					270		
Ser	Glu	Asp	Pro	Ile	Pro	Glu	Ser	Val	Ile	Gln	Asn	Tyr	Asn	Lys	Ala
		275					280					285			
Leu	Gln	Gln	Leu	Glu	Lys	Tyr	Lys	Pro	Tyr	Glu	Glu	Ala	Leu	Leu	Gln
	290					295					300				
Ala	Glu	Ala	Pro	Arg	Leu	Ala	Glu	Tyr	Gln	Ala	Tyr	Ile	Asp	Phe	Glu
305					310					315					320
Met	Lys	Ile	Gly	Asp	Pro	Ala	Arg	Ile	Gln	Leu	Ile	Phe	Glu	Arg	Ala
				325					330					335	
Leu	Val	Glu	Asn	Cys	Leu	Val	Pro	Asp	Leu	Trp	Ile	Arg	Tyr	Ser	Gln
			340					345					350		
Tyr	Leu	Asp	Arg	Gln	Leu	Lys	Val	Lys	Asp	Leu	Val	Leu	Ser	Val	His
		355					360					365			
Asn	Arg	Ala	Ile	Arg	Asn	Cys	Pro	Trp	Thr	Val	Ala	Leu	Trp	Ser	Arg

370	375	380
Tyr Leu Leu Ala Met Glu Arg His Gly Val Asp His Gln Val Ile Ser		
385	390	395
Val Thr Phe Glu Lys Ala Leu Asn Ala Gly Phe Ile Gln Ala Thr Asp		400
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Tyr Val Glu Ile Trp Gln Ala Tyr Leu Asp Tyr Leu Arg Arg Arg Val		415
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Asp Ser Ile Met Thr Arg Gly Asn Ala Lys Tyr Ala Asn Met Trp Leu		495
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Glu Tyr Tyr Asn Leu Glu Arg Ala His Gly Asp Thr Gln His Cys Arg		510
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Lys Ala Leu His Arg Ala Val Gln Cys Thr Ser Asp Tyr Pro Glu His		525
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Gln Glu Glu Glu Lys Ala Glu Gln Arg Lys Arg Ala Arg Ala Glu Lys		590
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Pro Ile Phe Ser Asn Arg Gly Asp Phe Arg Gly Tyr Cys Tyr Val Glu		735
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